

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Bowman, Michael
- (ii) TITLE OF INVENTION: SECRETED PROTEIN BA3.1 AND POLYNUCLEOTIDES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genetics Institute, Inc.
  - (B) STREET: 87 CambridgePark Drive
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Sprunger, Suzanne A.
  - (B) REGISTRATION NUMBER: 41,323
  - (C) REFERENCE/DOCKET NUMBER: G15295A
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (617) 498-8284
  - (B) TELEFAX: (617) 876-5851

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1086 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCGGTAC GATTGTGTAG ACACAGGAGA TGATCTTGAC CCTGATATCA TTAATATCCT	60
TCCTGCTTCT CCAACTGGTT CTCTGTACA TTCTCCAGGA TCTCATTACC CCCATGGAGG	120
TGATGCGGGC AAGGGTCAGA GTACTGATCG GCTACTATCA ACAGAACCTC ATGAGGAAGT	180
ACCTAATATT CTTCAGCAAC CATGCGCCT TGGTTACTTT GTATCAACTG CCAAAGCAGG	240
TCCATTACCT GACTGGTTCT GGTCAGCATG TCTCAAGCA CAATATCAGT GTCCCCTTT	300
TTCTTAAGGC CTCTTTGCAC CTCCACGTGC CTTCAGTGCA ATCTGACGAG CTGCTTCACA	360
GTAAACACTC CCACCCACTT GACTCAAATC AGACTTCAGA TGTCTCAGG TTTGTTTTGG	420

AACAGTACAA TGCACCTCC TGCTAACCT GTGACCCTGC AACCCAGGAC AGACGCTCAT 480  
 GTCTCCCAAT TCATTTTGTG GTGCTGAATC AGTTATATAA CTTTATTATG AATATGCTGT 540  
 GATCTTCATT TGATGGAAC GTGCAAGAAA AGARCAAGGA AAAATGGATG TTTCGTGCA 600  
 GGATTAAGTT ACAATTATCT TCTCAGTGAA GGTCAATTGT GATGGGGTCT AATTCCTATT 660  
 ACTTCAACAA ATATTGTTTT GACTTGGGGG GAGGGGCTAT AACCTGCTA TTTTTCATTG 720  
 ACTCTATTGA ACTCTTTAGG ATGATGACTG ATCATACAAA ACGTATTATA ACATTTTCGT 780  
 AGCAAAATTA ACCTTTTTTT TTTCCAGTCA CAGTATTGTG GAAAAGTAAT GAGCCATAGT 840  
 ACCCAGTCAT GTTAAATGAA TATTTAAAGC ATGGAGAGGA AACATGAGGA ACAATGAATT 900  
 TCAACATATG GCTTCAGAAC ATGAAGATGT TCTTGTATGG ATTATAGTAT CTAGTATTCA 960  
 AAAATGCCTG CATCTCTTCT CTTATTATT GTAGTTTTT AAATGTATAA ATTGTCTTAT 1020  
 ATTTCTTAAC CTCCTTTTATA AAAATTTTCC TAGAAGGTTT ATACTGCCAA AAAAAA 1080  
 AAAAAA 1086

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ile Leu Thr Leu Ile Ser Leu Ile Ser Phe Leu Leu Leu Leu 15  
 1 5 10  
 Val Leu Leu Tyr Ile Leu Gln Asp Leu Ile Thr Pro Met Glu Val Met 30  
 20 25 30  
 Arg Ala Arg Val Arg Val Leu Ile Gly Tyr Tyr Gln Gln Asn Leu Met 45  
 35 40 45  
 Arg Lys Tyr Leu Ile Phe Phe Ser Asn His Trp Pro Leu Val Thr Leu 60  
 50 55 60  
 Tyr Gln Leu Pro Lys Gln Val His Tyr Leu Thr Gly Ser Gly Gln His 80  
 65 70 75 80  
 Val Leu Lys His Asn Ile Ser Val Pro Phe Phe Leu Lys Ala Ser Leu 95  
 85 90 95  
 His Leu His Val Pro Ser Val Gln Ser Asp Glu Leu Leu His Ser Lys 110  
 100 105 110  
 His Ser His Pro Leu Asp Ser Asn Gln Thr Ser Asp Val Leu Arg Phe 125  
 115 120 125  
 Val Leu Glu Gln Tyr Asn Ala Leu Ser Trp Leu Thr Cys Asp Pro Ala 140  
 130 135 140  
 Thr Gln Asp Arg Arg Ser Cys Leu Pro Ile His Phe Val Val Leu Asn 160  
 145 150 155 160  
 Gln Leu Tyr Asn Phe Ile Met Asn Met Leu 170  
 165 170